

FIG. 1 A(1)

Title: NOVEL RECEPTOR-TYPE
PHOSPHOTYROSINE PHOSPHATASE-ALPHA
Inventor(s): Joseph SCHLESSINGER et al.
Appl. No.: Unassigned

FIG. 1A (2)

Title: NOVEL RECEPTOR-TYPE
 PHOSPHOTYROSINE PHOSPHATASE-ALPHA
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1030 ctc caagg aaacaagg aaacaaccg cctatgt aaacatccctg cccatgt aaccactct tagt gacccatctt 1050
 S K E N K E I K N R Y V N I L P Y D H S R V H L T P V E
 1110 aagg ggtccaggatttcatcaacgcttcatttcattaaatggcttaccaggaaaagaaacaattcatcgcttgcacaaggac
 G V P D S D Y I N A S F I N G Y Q E K N K F I A A Q G P
 1190 caaaaggaaacagtgaatgtgacttctggagaatgtggaaacaaacacagctactattgtcatgggtgacccaaacctgaaagg
 K E E T V N D F W R M I W E Q N T A T I V M V T N L K E
 1270 agagaaaggaggtaatgtgcccataacttggccagaccaccaaggctgtggaccctatggaaatgtccgtgtatgtcgaggatg
 R K E C K C A Q Y W P D Q G C W T Y G N V R V S V E D V
 1350 tgactgttctggactacacagtacggaaaattctcgatccagggtggccgacgtgaccaacaggaaaccacagcgccatcat
 F V L V D Y T V R K F S I Q Q V G D V T N R K P Q R L I
 1370 1430
 1450 cactcaggccacttccaccaggccaggactttgggtgccttcaccccaattggcatgtcaagttcctcaagaagggtgaaag
 T Q F H F T S W P D F G V P F T P I G M L K F L K V K
 1530 1510
 1550 gcctgttaaccctcaggtaacggccaggctatcggttccactcgcaagtggatgtgggttgcagggttgcggcactggcac
 A C N P Q Y A G A I V V H C S A G V G R T G T F V V I D A
 1610 1590
 1630 ccatgtggacatgtcggaggccaaagtggatgttatatgggtttgtggccggatccggccagggttgc
 M L D M H S E R K V D V Y G F V S R I R A Q R C M V
 1690 1670
 1710 cagacagacatgtcggaggacttccatataccaggcccttctggaggattatctgttatggggacacagaactggaaat
 Q T D M Q Y V F I Y] Q A L L E H Y L Y G D T E L E V T S L
 1730 1750
 1790 tagaaaaaccctaaaaattataacaagatccaggacttagcaacaacacgggttagaggaggatttaaagaattaaacttc
 E T H L Q K I Y N K I P G T S N N G L E E F K K L T S
 1870 1850
 1890 aatccaaatccagaatgtggaggaaacccatggccaaacatgtggaaacccatggggatccat
 I K I Q N D K M R T G N L P A N M K I K N R V L Q T I P Y
 1950 1990
 1970 gaatttaacagaggatgttccaggtaacccaggccaaacggggccaaacatgtggatccat
 E F N R V I I P V K R G E E N T D Y V N A S F I D G Y R Q
 2010

FIG. 1A(3)

FIG. 1 B

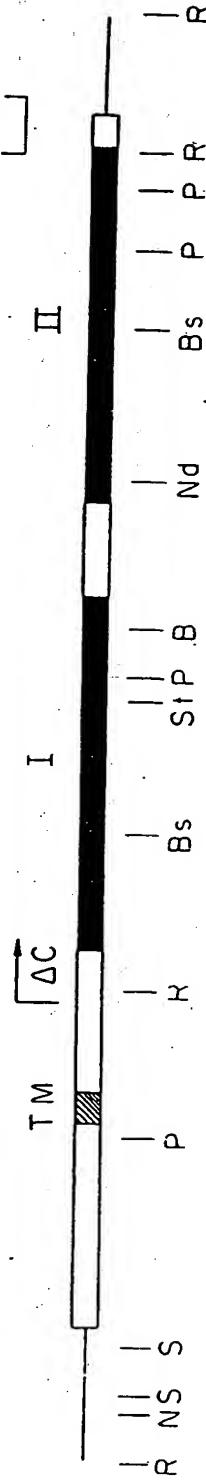


FIG. 2

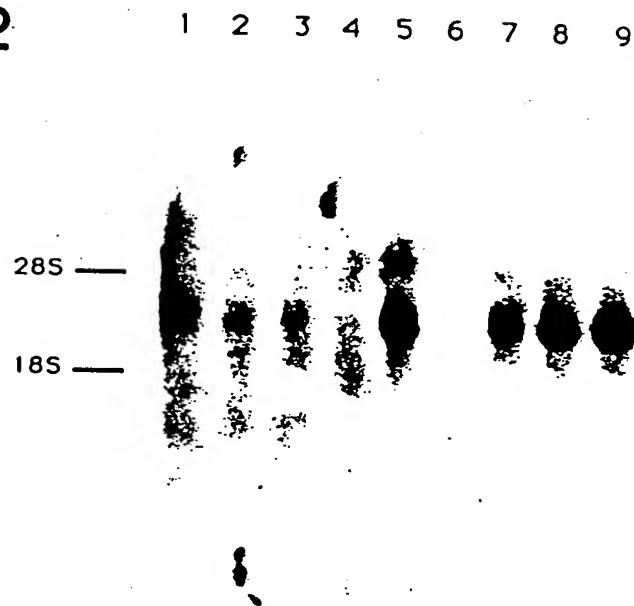
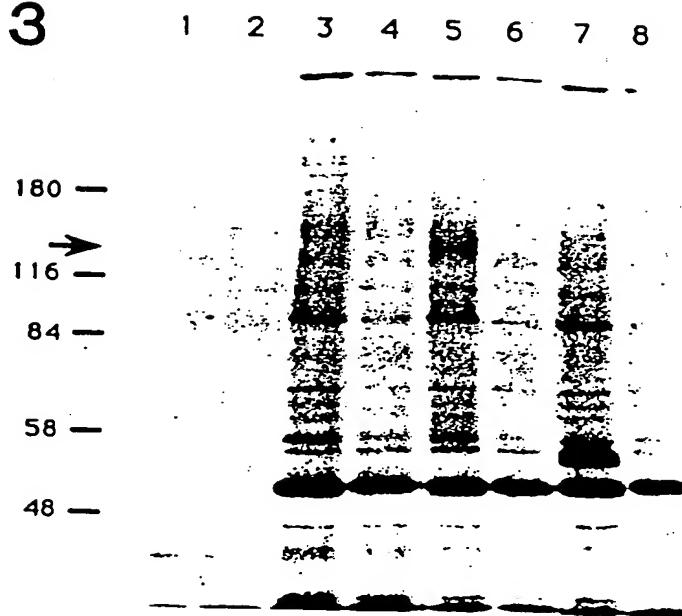
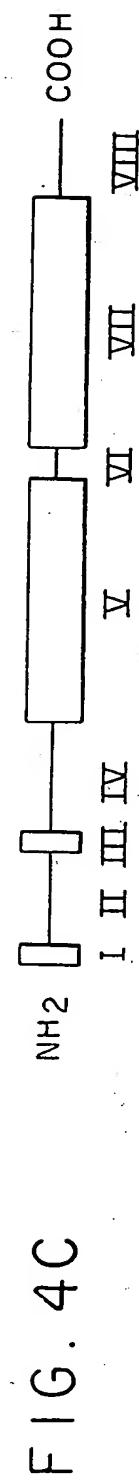
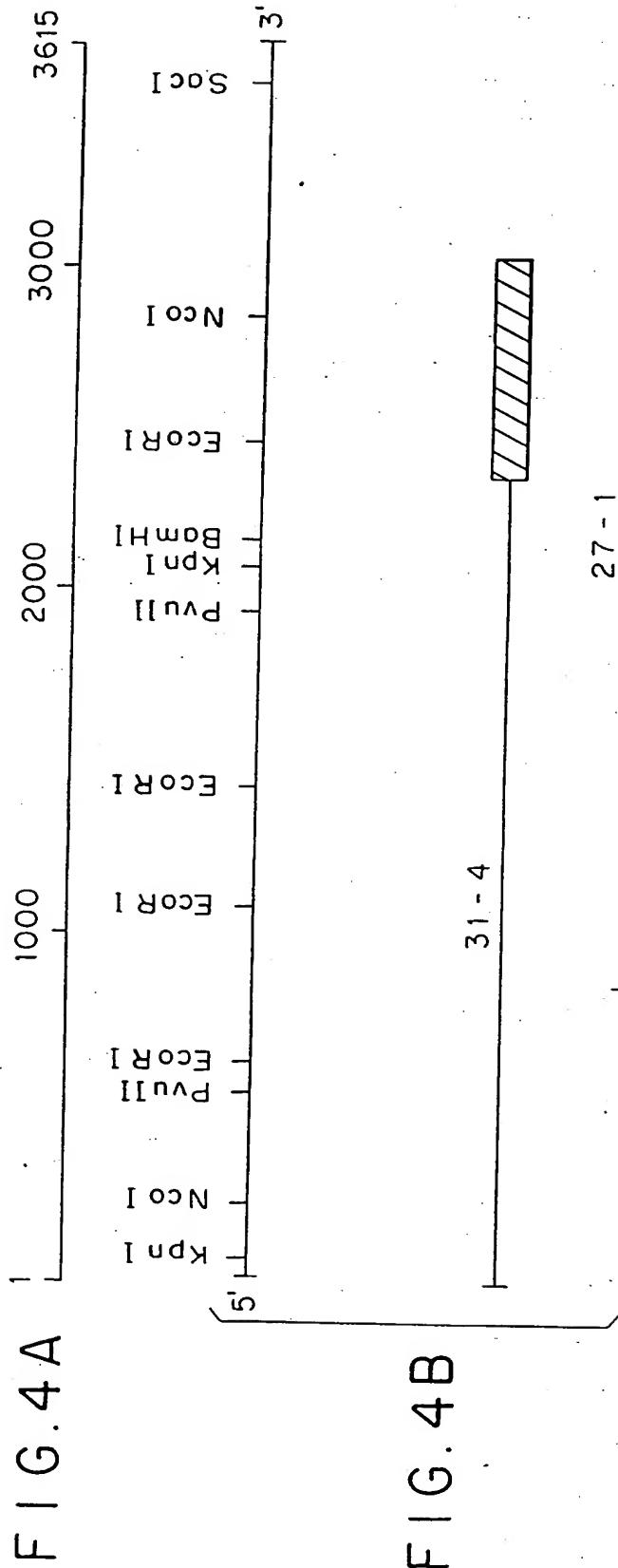


FIG. 3





F I G. 4 D

Title: NOVEL RECEPTOR-TYPE
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① [MDSWFILVLLGSGLICVS] ANNATVAPSVGGITRLINNSSTAEPVKEEAKTSNPTSSILTSVAPTFSP 68
2 F H S L T KT T LA N S VI 68

1 NITLGPTYLTTVNSSDSDNGTTRASTNSIGITISPNGT¹⁰WLPDNQFTDARTEPWEGNSSTAATTPETFP 136
2 L E V H R A E G T S IE I 136

1 PSGNSDSKDRD¹¹⁰EPIIAWVALSSLLVIVFIIIVLYM¹¹⁵TRFKKYKQAGSHNSFRLSNGRTEDVEPQS 204
2 A----- 195

1 VPLARSPTNRYKPLPVDKLEEINRRMADDNKLFREEFNALPACPIQATCEAASKEEENKEKNRYV 272
2

1 NILPYDHSRVHLTPVEGVPDSDYINASFINGYQEKNKFLIAAGPKEETVNDFWRMIWEQNTATTIVMVT 340
2

1 NLKERKECKCAQXYWPDQGCTYGNIRVSVEDVTVLVDYTVRKFCIQQVGDMTNRKPQLITQFHFTSW 408
2 V S V 399

1 PDFGVPPFTPIGMLKFLKKVKACNPQYAGAIIVVHCSAGVGRGTGTVVVIDAMLDMMHTERKVVDVYGFTVSR 476
2 S

1 IRAQRCQMVQTDQYVFTYQALLEHTLYGDTLEVTSLETHLQKIYKIPGTNSNNGLEEEFKLTSIK 544
2

1 IQNDKMRGNLPPANMKKNRVLQIIPYEFNRVIIIPVKRGEENTDYNASFIDGYRQKDSYIASQGPLIH 612
2

1 TIEDFWRMWIWEWKSCSIVMLTEERGQEKCAQYWPSDGLVSYGDTITVELKKEEECESYTVRDLLVVTN 603
2

1 TRENKSRQIROFHEHGWPEVGIPSDGKGMISIIIAAVQKQQQSGNHPITVHCSAGAGRIGTFCALSTV 671
2 N

1 LERVKAEGILDVVFOTVKSRLQRPHTVQTLQEYFCYKVQEXYDADFSDYANFK 748
2

1 802
2 793

FIG. 5A

LCA	NqnKNRYVdILPYDynRVeL	sEinGdagSnyINASyIdGfkEprKyIAA	10 20 30 40
RPTPase α	NKeKNRYVNILPYDlISRVhLtpvE	GvpdSDYINASfInGYqEknKfIAA	
RPTPase β	NKHKNRYINIVAYDHSRVKLaqLaeKDgKl	tDYINANYVDGYNrpkAYIAA	
RPTPase γ	NKHKNRYINILAYDHSRVKLrpLpgKDskhs	DYINANYVDGYNkaKAYIAAt	
CON	NkhKNRY-nIl-YDhsRVkL--l--k--k-sdYINA-y-dGynePK-yIAa		
LCA	QGPrdETVdDFWRMIWEQkAtvIVMVTrceEgnrnKCAeYWPsMeegTra	50 60 70 80 90	
RPTPase α	QGPkeETVnDFWRMIWEQntatIVMVTNLkErkecKCAQYWPdqGewTYG		
RPTPase β	QGPLKStaEDFWRMIWEhNnevIVMITNLVEKGRKCDQYWPadGSEEVG		
RPTPase γ	QGPLKStfEDFWRMIWEqNtgiIVMITNLVEKGRKCDQYWPtenSEEVG		
CON	QGPLk-TveDFWRMIWEqnt-vIVM-TnlvEkgrrKC-qYWP--gse-yg		
LCA	fgdVvVkinghkrcpDYiiqKl	100 110 120 nIvn 130	
RPTPase α	NirVsVedVtVLv	DYTVRKFc	kkekAtgRevThiq
RPTPase β	NflVTqKSVqVLA	yYTvrNftlRNTKIKK	mtnRkpqRliTQfH
RPTPase γ	NiivTlKStkihAc	Gs	qKGRpsgRVVTQYH
CON	ni-Vtvk-v-vla--dYtvrkf--rntki-k-g-k---kgr--gRvvtqyh		
LCA	FTSWPDhGVPedPhllLKlrrVnAfsnffsGpIVVHCSAGVGRTGTYigID	140 150 160 170 180 190	
RPTPase α	FTSWPDfGVPftPigmLKf1kKVkAcnpqyaGaIVVHCSAGVGRTGTFvVID		
RPTPase β	YTQWPDMGVPEYsLPVLTFVRKaayAkrhavGPVVVHCSAGVGRTGTYIVlD		
RPTPase γ	YTQWPDMGVPEYsLPVLTFVRrssaArmpetGPV1VHCSAGVGRTGTYIVlD		
CON	-T-WPDmGVPeyp1pvL-fvr-v-aa----Gp-vVHCSAGVGRTGTYiviD		
LCA	AMLegleaEnKVDVYGYVvk1RrQRC1MVQveaQYilihQALvE	200 210 220 230	
RPTPase α	AMLdmuhhtErKVDVYGFVsrIRaQRCqMVQTdmQYVF1yQAL1E		
RPTPase β	SMLQQIqhEgTVNifGFLKHIRsQRNYLVQTEEQYVFIHDtLvE		
RPTPase γ	SMLQQIkdkstVNv1GFLKHIRtQRNYLVQTEEQYiFIHDaL1E		
CON	-MLqqi--e--v-vyGf-khiR-QR-y-VQteeQY-fIh-aL-E		

F I G . 5 B (1)

	10	20	30	40		
LCA	NksKNRnsnvIPYdyNRVplkhelemskesehdsdessdddssdsEEpsky					
RPTPase α	NmkKNRvlqlIIPYEfNRViIpvr				GEEenTDY	
RPTPase β	NrEKNRtSSIIIPvERsRVGIssLs				GE GTDY	
RPTPase γ	NkEKNRnSSvvPsERaRVGlapLp				GmkGTDY	
CON	NkeKNRnss-iPyernRVg---l-----geegtdy					
	50	60	70	80	90	
LCA	iNASFImSYwkpevmIAaQGPLkeTigDFWqMIfqrKvkvIVMLTELkhg					
RPTPase α	vNASFIdGYrQkdsyIASQGPLLHTIeDFWRMIWewKscsIVMLTELeer					
RPTPase β	INASYIMGGYQSNIFIITQHPLLHTIKDFWRMIWDHNAQlVVMiPDgQnm					
RPTPase γ	INASYIMGGYrSNEFIITQHPLpHTtKDFWRMIWDHNAQiiVMLPDnQsl					
CON	iNAS-ImgYyqsnefI-tQ-PLlhTikDFWrMIwdh-naqiVml---q--					
	100	110	120	130	140	
LCA	dQEiCAQYW geGkqtYGDIEvdLKdtdksstYTl RvfelrhskrkdSRtv					
RPTPase α	gQEKAQYWPsdlvSYGDI tVeLKkeeeCESYTV RdllvtntreNkSRqI					
RPTPase β	A EDEFVYWPn kDEpi NCESFkVTLmaehkCLSNEEkli					
RPTPase γ	A EDEFVYWPn reEsm NCEaFtVTLiskdr1CLSNEEqiI					
CON	aE-e--qYWps-g---ygd--v-1k---nces-tvt---e-r-clsne-r-i					
	150		160	170	180	
LCA	YQY qY tnWsvéqlP aepKeliSmIqvVkQKlpQk					
RPTPase α	rQf HF hgWPevgiP SdgKgmISiIaaV Qk Qq					
RPTPase β	IQDFILEATQDDYVLEVRHFQCPKWPNPDSPIskTFELISVI					K
RPTPase γ	IhDFILEATQDDYVLEVRHFQCPKWPNPDAPISSkTFELINVI					K
CON	iqdfileatqddyvlevrhfqcpkWpnPD-Pis-t-elisvI-----qk					

F I G . 5 B (2)

LCA	190	200	210	220	230
	nsseGNkhhkstP1liHCrdGsqqTG1FCALlnlL	saetEevvDiFQvVKa			
RPTPase α	qqSGNh	PitVHCsaGagrTGTFCALsTvLERvkaEgilDVfQtvKs			
RPTPase β	EEAaNR	DGPmIVHDEhGgVtAGTFCALTTLmhOLEkENSVDVyQVAKM			
RPTPase γ	EEAltR	DGPtIVHDEyGaVsAGmlCALTTLsqQLEnENaVDVfQVAKM			
CON	-eea-nr---dgP-ivH-e-Gav--GtfCALttlgle-En-vDvfQv-Km				
LCA	240	250			
	LrkaRPgMVstfEQYqF1YdVias				
RPTPase α	LaLqRPhMVqT1EQYeFcYKVvqe				
RPTPase β	INLMRPGVFaDIEQYQF1YKVils				
RPTPase γ	INLMRPGVftDIEQYQFIYkarLS				
CON	-nlmRPg----iEQYqF1Ykvils				

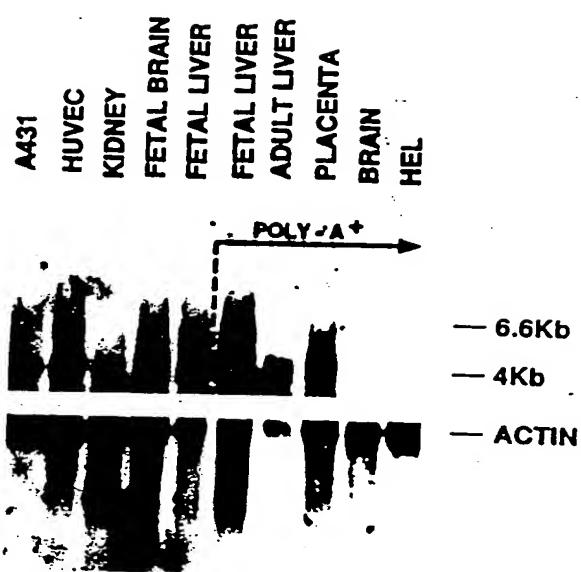


FIG. 6

FIG. 7

HUMAN CHROMOSOMES

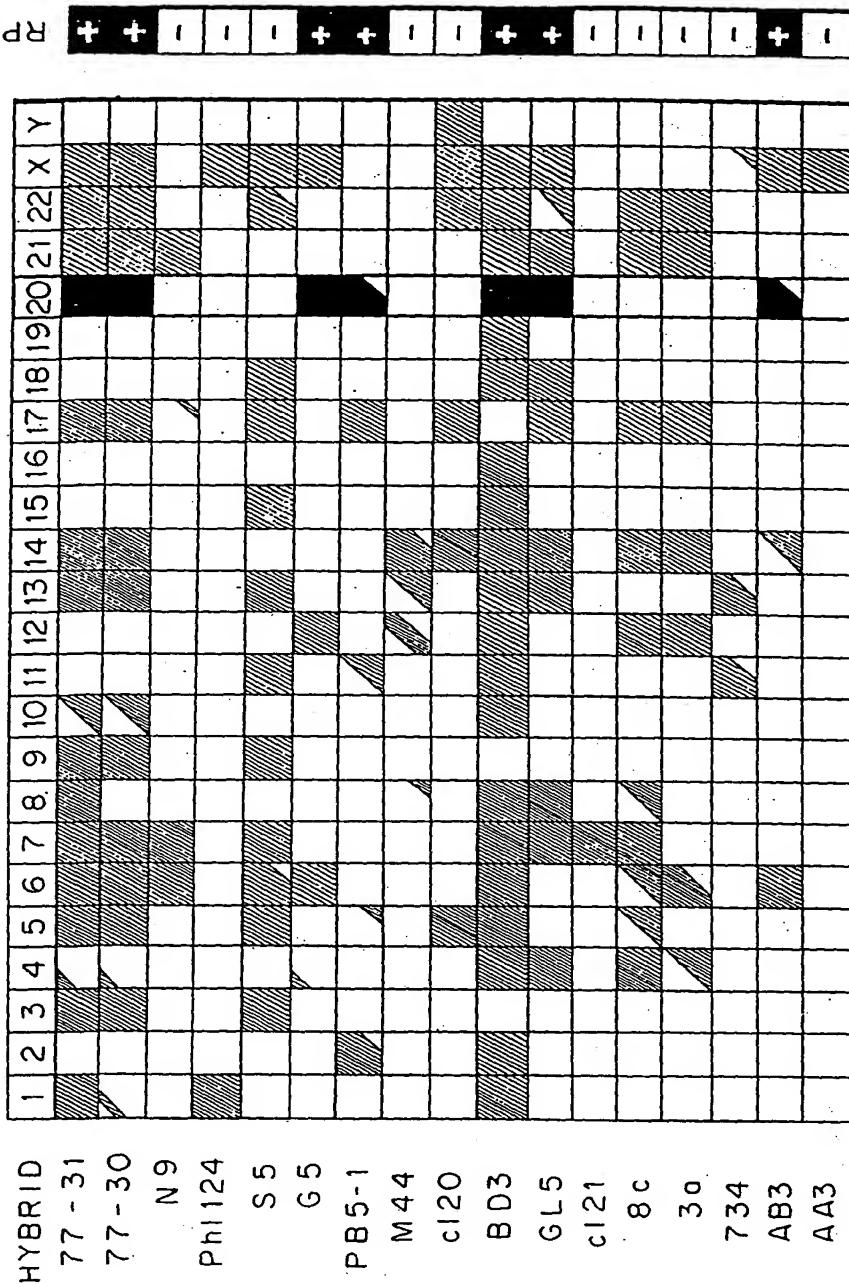


FIG. 8 (1)

1	ATGGATTCTGGTTCATTCTTGTCTGCTCGGCAGTGGTCTGATATGTGTCAGTGCAAC	60
1	M D S W F I L V L L G S G L I C V S A N	20
61	AATGCTACCACAGTTGCACCTCTGTAGGAATTACAAGATTAATTAACTCATCAACGGCA	120
21	N A T T V A P S V G I T R L I N S S T A	40
121	GAACCAGTTAAGAAGAGGCCAAAACCTCAAATCCAACCTCTCACTAACTCTCTTCT	180
41	E P V K E E A K T S N P T S S L T S L S	60
181	GTGGCACCAACATTCAAGCCAAATATAACTCTGGGACCCACCTATTTAACCACTGTCAAT	240
61	V A P T F S P N I T L G P T Y L T T V N	80
241	TCTTCAGACTCTGACAATGGGACCACAAGAACAGCAAGCACCATTCTATAGGCATTACA	300
81	S S D S D N G T T R T A S T N S I G I T	100
301	ATTTCACCAAATGGAACGTGGCTTCCAGATAACCAGTTCACGGATGCCAGAACAGAACCC	360
101	I S P N G T W L P D N Q F T D A R T E P	120
361	TGGGAGGGAAATTCCAGCACCGCAGCAACCAACTCCAGAAACTTTCCCTCCTCAGGTAAT	420
121	W E G N S S T A A T T P E T F P P S G N	140
421	TCTGACTCGAAGGACAGAACAGAGATGAGACACCAATTATTCGGTGATGGTGGCCCTGTCC	480
141	S D S K D R R D E T P I I A V M V A L S	160
481	TCTCTGCTAGTGATCGTGTATTATCATAGTTTGTACATGTTAGGTTAACGAAATAC	540
161	S L L V I V F I I I V L Y M L R F K K Y	180
541	AAGCAAGCTGGGAGCCATTCCAATTCTTCCGCTTATCCAACGGCCACTGAGGATGTG	600
181	K Q A G S H S N S F R L S N G R T E D V	200
601	GAGCCCCAGAGTGTGCCACTCTGGCCAGATCCCCAACGCACCAACAGGAAATAACCCACCC	660
201	E P Q S V P L L A R S P S T N R K Y P P	220
661	CTGCCCGTGGACAAGCTGGAAAGAGGAAATTAAACCGGAGAATGCCAGACGACAATAAGCTC	720
221	L P V D K L E E E I N R R M A D D N K L	240
721	TTCAGGGAGGAATTCAACGCTCTCCCTGCATGTCCTATCCAGGCCACCTGTGAGGCTGCT	780
241	F R E E F N A L P A C P I Q A T C E A A	260
781	TCCAAGGAGGAAAACAAGGAAAAATCGATATGTAACATCTTGCCATTGACCACTCT	840
261	S K E E N K E K N R Y V N I L P Y D H S	280

FIG. 8 (2)

841	AGAGTCCACCTGACACCGGTTGAAGGGGTTCCAGATTCTGATTACATCAATGCTTCATTC	900
281	R V H L T P V E G V P D S D Y I N A S F	300
901	ATCAACGGTACCAAGAAAAGAACAAATTCAATTGCTGCACAAGGACCAAAAGAACG	960
301	I N G Y Q E K N K F I A A Q G P K E E T	320
961	GTGAATGATTTCTGGCGGATGATCTGGGAACAAAACACAGCCACCATCGTCATGGTTACC	1020
321	V N D F W R M I W E Q N T A T I V M V T	340
1021	AACCTGAAGGAGAGAAAGGAGTGCAGTGCCAGTACTGGCCAGACCAAGGCTGCTGG	1080
341	N L K E R K E C K C A Q Y W P D Q G C W	360
1081	ACCTATGGGAATATTGGGTGTCGTAGAGGATGTGACTGTCTGGTGGACTACACAGTA	1140
361	T Y G N I R V S V E D V T V L V D Y T V	380
1141	CGGAAGTTCTGCATCCAGCAGGTGGCGACATGACCAACAGAAAGCCACAGCGCCTCATC	1200
381	R K F C I Q Q V G D M T N R K P Q R L I	400
1201	ACTCAGTTCCACTTACCAAGCTGCCAGACTTGGGGTGCCTTTACCCGATGGCATG	1260
401	T Q F H F T S W P D F G V P F T P I G M	420
1261	CTCAAGTTCCCTCAAGAAGGTGAAGGCCTGTAACCCCTCAGTATGCAGGGGCCATCGTGGTC	1320
421	L K F L K K V K A C N P Q Y A G A I V V	440
1321	CACTGCAGTGCAGGTGAGGGCGTACAGGTACCTTGTGTCATTGATGCCATGCTGGAC	1380
441	H C S A G V G R T G T F V V I D A M L D	460
1381	ATGATGCATACAGAACCGAACGGTGGACGTATGGCTTGTGAGCCGGATCCGGCACAG	1440
461	M M H T E R K V D V Y G F V S R I R A Q	480
1441	CGCTGCCAGATGGTCAAACCGATATGCAGTATGTCTTCATATACCAAGCCCTCTGGAG	1500
481	R C Q M V Q T D M Q Y V F I Y Q A L L E	500
1501	CATTATCTATGGAGATAAGAACACTGGAAAGTGACCTCTCTAGAAACCCACCTGCAGAAA	1560
501	H Y L Y G D T E L E V T S L E T H L Q K	520
1561	ATTTACAACAAATCCCAGGGACCAGCAACAAATGGATTAGAGGAGGAGTTAAGAACTTA	1620
521	I Y N K I P G T S N N G L E E E F K K L	540
1621	ACATCAATCAAATCCAGAGATGACAAGATGCCAGTGGAAACCTCCAGCCACATGAAG	1680
541	T S I K I Q N D K M R T G N L P A N M K	560
1681	AAGAACCGTGTACAGATCATTCCATATGAATTCAACAGAGTGTGATCATTCCAGTTAAG	1740
561	K N R V L Q I I P Y E F N R V I I P V K	580

FIG. 8 (3)

1741	CGGGCGAAGAGAATACAGACTATGTGACCGCATCCTTATTGATGGCTACCGGCAGAAG	1800
581	R G E E N T D Y V N A S F I D G Y R Q K	600
1801	GACTCCTATATGCCAGCCAGGGCCCTCTCTCCACACAATTGAGGACTTCTGGCGAATG	1860
601	D S Y I A S Q G P L L H T I E D F W R M	620
1861	ATCTGGGAGTGGAAATCTGCTCTATCGTATGGCTAACAGAACTGGAGGAGAGAGGCCAG	1920
621	I W E W . K S C S I V M L T E L E E R G Q	640
1921	GAGAAGTGTGCCAGTACTGCCATCTGATGGACTGGTGTCCATGGAGATATTACAGTG	1980
641	E K C A Q Y W P S D G L V S Y G D I T V	660
1981	GAACGTGAAAGGAGGAGGAATGTGAGAGCTACACCGTCCGAGACCTCCTGGTCACCAAC	2040
661	E L K K E E E C E S Y T V R D L L V T N	680
2041	ACCAGGGAGAATAAGAGCCGGCAGATCCGGCAGTTCCACTTCCATGGCTGGCTGAAGTG	2100
681	T R E N K S R Q I R Q F H F H G W P E V	700
2101	GGCATCCCCAGTGACGGAAAGGGCATGATCAGCATCATGCCGCCGTGCAGAACAGCAG	2160
701	G I P S D G K G M I S I I A A V Q K Q Q	720
2161	CAGCAGTCAGGGAAACCACCCATCACCGTGCCTGCAGCGCCGGGCAGGAAGGACGGGG	2220
721	Q Q S G N H P I T V H C S A G A G R T G	740
2221	ACCTTCTGTGCCCTGAGCACCGTCTGGAGCGTGTGAAAGCAGAGGGATTTGGATGTC	2280
741	T F C A L S T V L E R V K A E G I L D V	760
2281	TTCCAGACTGTCAAGAGCCTGCGGCTACAGAGGCCACACATGGTCAGACACTGGAACAG	2340
761	F Q T V K S L R L Q R P H M V Q T L E Q	780
2341	TATGAGTTCTGCTACAAGGTGGTGCAGGAGTATATTGATGCATTCTCAGATTATGCCAAC	2400
781	Y E F C Y K V V Q E Y I D A F S D Y A N	800
2401	TTCAAGTAA 2409	
801	F K * 803	